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	<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ</i>		
<input type="checkbox"/>	L16	MEGF10	1
<input type="checkbox"/>	L15	human EGF	909
<input type="checkbox"/>	L14	L13 AND MEGF10	0
<input type="checkbox"/>	L13	L12 AND human	2057
<input type="checkbox"/>	L12	L11 AND EGF	2067
<input type="checkbox"/>	L11	536/23.1,23.4,23.5.CCLS.	17622
<input type="checkbox"/>	L10	L9 AND MEGF10	1
<input type="checkbox"/>	L9	L8 AND human	2819
<input type="checkbox"/>	L8	L7 AND EGF	2828
<input type="checkbox"/>	L7	435/325.CCLS.	14916
<input type="checkbox"/>	L6	Maranda-M.IN.	1
<input type="checkbox"/>	L5	Miranda-Maricar.IN.	22
<input type="checkbox"/>	L4	Miranda.IN.	911
<input type="checkbox"/>	L3	Yu-X.IN.	546
<input type="checkbox"/>	L2	Yu-Xuanchuan.IN.	22
<input type="checkbox"/>	L1	(Yu.IN.)	87877

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L2 13DUP REM L1 (3 DUPLICATES REMOVED)

=> D L2 1-13

L2 ANSWER 1 OF 13 USPATFULL on STN
AN 2004:7325 USPATFULL
TI Proteins, polynucleotides encoding them and methods of using the same
IN Anderson, David W., Branford, CT, UNITED STATES
Burgess, Catherine E., Wethersfield, CT, UNITED STATES
Caskan, Stacie J., North Haven, CT, UNITED STATES
Colman, Steven D., Guilford, CT, UNITED STATES
Edinger, Shlomit R., New Haven, CT, UNITED STATES
Ellerman, Karen, Branford, CT, UNITED STATES
Gerlach, Valerie, Branford, CT, UNITED STATES
Gunther, Erik, Branford, CT, UNITED STATES
Kekuda, Ramesh, Stamford, CT, UNITED STATES
MacDougall, John R., Hamden, CT, UNITED STATES
Mehraban, Fuad, Trumbull, CT, UNITED STATES
Patturajan, Meera, Branford, CT, UNITED STATES
Rothenberg, Mark, Clinton, CT, UNITED STATES
Shimkets, Richard A., Guilford, CT, UNITED STATES
Smithson, Glenda, Guilford, CT, UNITED STATES
Spytek, Kimberly A., New Haven, CT, UNITED STATES
Stone, David J., Guilford, CT, UNITED STATES
Vernet, Corine A.M., Branford, CT, UNITED STATES
Zerhusen, Bryan D., Branford, CT, UNITED STATES
PI US 2004005558 A1 20040108
AI US 2002-52648 A1 20020118 (10)
PRAI US 2001-262454P 20010118 (60)
US 2001-272920P 20010302 (60)
US 2001-284549P 20010418 (60)
US 2001-303229P 20010705 (60)
US 2001-262892P 20010119 (60)
US 2001-263605P 20010123 (60)
US 2001-269098P 20010215 (60)
US 2001-264159P 20010125 (60)
US 2001-265517P 20010131 (60)
US 2001-271855P 20010227 (60)
US 2001-267057P 20010207 (60)
US 2001-286287P 20010425 (60)
DT Utility
FS APPLICATION
LN.CNT 10349
INCL INCLM: 435/006.000
INCLS: 435/007.200; 435/069.100; 435/320.100; 435/325.000; 514/012.000;
514/044.000; 530/350.000; 530/388.100
NCL NCLM: 435/006.000
NCLS: 435/007.200; 435/069.100; 435/320.100; 435/325.000; 514/012.000;
514/044.000; 530/350.000; 530/388.100
IC [7]
ICM: C12Q001-68
ICS: G01N033-53; G01N033-567; A61K038-17; A61K048-00; C12P021-02;
C12N005-06; C07K014-47; C07K016-18
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L2 ANSWER 2 OF 13 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 1
AN 2001:330391 CAPLUS
DN 136:64933
TI Prediction of the coding sequences of unidentified human genes. XX. The
complete sequences of 100 new cDNA clones from brain which code for large
proteins in vitro
AU Nagase, Takahiro; Nakayama, Manabu; Nakajima, Daisuke; Kikuno, Reiko;
Ohara, Osamu
CS Kazusa DNA Research Institute, Chiba, 292-0812, Japan
SO DNA Research (2001), 8(2), 85-95
CODEN: DARSE8; ISSN: 1340-2838
PB Universal Academy Press
DT Journal
LA English
RE.CNT 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 3 OF 13 LIFESCI COPYRIGHT 2004 CSA on STN
AN 2004:35501 LIFESCI
TI Prediction of the Coding Sequences of Unidentified Human Genes. XX. The
Complete Sequences of 100 New cDNA Clones from Brain which Code for Large
Proteins in vitro
AU Nagase, T.; Nakayama, M.; Nakajima, D.; Kikuno, R.; Ohara, O.

CS Kazusa DNA Research Institute, 1532-3 Yana, Kisarazu, Chiba 292-0812,
Japan
SO DNA Research [DNA Res.], (20010000) vol. 8, [np].
ISSN: 1340-2838.
DT Journal
FS N
LA English
SL English

L2 ANSWER 4 OF 13 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
AN AAL52376 DNA DGENE
TI New epidermal growth factor producing Lactococcus lactis or Lactococcus
casei, useful for promoting gut adsorption or for treating Short Bowel
Syndrome.
IN Steidler L
PA (VLAA-N) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
(UYGE-N) UNIV GENT.
PI WO 2004001020 A2 20031231
AI WO 2003-EP50242 20030619
PRAI EP 2002-77532 20020619
DT Patent
LA English
OS 2004-071734 [07]
DESC Murine epidermal growth factor coding sequence oligo ***MEGF10*** .

L2 ANSWER 5 OF 13 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): CK656927 GenBank (R)
GenBank ACC. NO. (GBN): CK656927
GenBank VERSION (VER): CK656927.1 GI:44893777
CAS REGISTRY NO. (RN): 660084-00-4
SEQUENCE LENGTH (SQL): 483
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 3 Mar 2004
DEFINITION (DEF): 3017HFEX25F2 BgORESTES schistosome-exposed NHM 3017
Head/foot 2 Biomphalaria glabrata cDNA clone ZBA0961
similar to ***MEGF10*** protein, mRNA sequence.

KEYWORDS (ST): EST
SOURCE: Biomphalaria glabrata (bloodfluke planorb)
ORGANISM (ORGN): Biomphalaria glabrata
Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata;
Basommatophora; Lymnaeidae; Planorbidae; Biomphalaria

COMMENT:
Contact: Lockyer, A.E.
Wolfson Wellcome Biomedical Laboratory
The Natural History Museum
Cromwell Road, London, SW7 5BD, UK
Tel: +44 (0)20 7942 5148
Fax: +44 (0)20 7942 5518
Email: a.lockyer@nhm.ac.uk
High quality sequence stop: 483
POLYA=No.

REFERENCE: 1 (bases 1 to 483)
AUTHOR (AU): Lockyer, A.E.; Spinks, J.N.; Kane, R.A.; Dias Neto, E.;
Noble, L.R.; Rollinson, D.; Jones, C.S.
TITLE (TI): ESTs from Biomphalaria glabrata using the ORESTES
approach
JOURNAL (SO): Unpublished (2003)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..483	/organism="Biomphalaria glabrata" /mol-type="mRNA" /strain="NHM 3017" /db-xref="taxon:6526" /clone="ZBA0961" /sex="Hermaphrodite" /tissue-type="Head/foot" /clone-lib="BgORESTES schistosome-exposed NHM 3017 Head/foot 2" /note="Vector: pGEM; mRNA, extracted from schistosome-exposed 3017 (resistant) snails was used"

as a template for RT-PCR with random primers to generate cDNA fragments. These were cloned and sequenced using M13F. Primer sequences were removed from sequence."

SEQUENCE (SEQ):

```
1 ggtcagaact gttccaatgt ctgccaatgt gatgtcagta attctctaaa ctgtaatgat
61 gtcgatggta catgcacttg taaaactggc tggactggaa ccaactgtga acaggacata
121 gatgagtgtg ctattaatgt aacattctgc tcaaactctt atgaagtttg ccgcaatgtg
181 aagggctctg cggaatgtat ttgtcaagat gggtttctaca attcaacaat tttattcagt
241 tgtcaagcct gtgactctct ccactatgga tcaaactgca cctctgtatg ctcatgtcat
301 acaaccaaca cagcagattg taatgatgtc aatggaacat gttcttgtaa acctggatgg
361 actggggctg attgctcgca aggttgatg tccctgcact atgggtcaaga ctgcaccttg
421 caatgtaa atgtcagttaaa taacagcgct gtatgcaata gcactgatgg aactgcaca
481 tgt
```

L2 ANSWER 6 OF 13 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): CD648703 GenBank (R)
GenBank ACC. NO. (GBN): CD648703
GenBank VERSION (VER): CD648703.1 GI:31905003
CAS REGISTRY NO. (RN): 537522-34-2
SEQUENCE LENGTH (SQL): 801
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 18 Jun 2003
DEFINITION (DEF): AUF_103_I07_T7 Crassostrea virginica Gill Crassostrea virginica cDNA 5' similar to ***MEGF10*** protein, mRNA sequence.

KEYWORDS (ST): EST
SOURCE: Crassostrea virginica (eastern oyster)
ORGANISM (ORGN): Crassostrea virginica
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Ostreoida; Ostreoidea; Ostreidae; Crassostrea

NUCLEIC ACID COUNT (NA): 253 a 130 c 157 g 261 t

COMMENT:

Contact: Liu ZJ
The Fish Molecular Genetics and Biotechnology Laboratory,
Department of Fisheries and Allied Aquacultures and Program of Cell
and Molecular Biosciences
Auburn University
203 Swingle Hall, Auburn University, Auburn, AL 36849, USA
Tel: 334 844 4054
Fax: 334 844 9208
Email: zliu@acesag.auburn.edu
Seq primer: M13 Reverse.

REFERENCE: 1 (bases 1 to 801)
AUTHOR (AU): Peatman,E.; Kucuktas,H.; Li,P.; He,C.; Feng,J.; Wei,X.;
Liu,Z.
TITLE (TI): Differentially expressed oyster (Crassostrea virginica)
genes after exposure to mercury
JOURNAL (SO): Unpublished

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..801	/organism="Crassostrea virginica" /mol-type="mRNA" /db-xref="taxon:6565" /clone-lib="Crassostrea virginica Gill" /note="Organ: Gill; Vector: psport1; Site-1: NotI; Site-2: SalI"

SEQUENCE (SEQ):

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1 gtttttgctt agaagcggat gggtaatcgg gtacattttc tgaactgggtg gtgatagggtg
61 ctttctgtag atgtgtgatg gcatataaac gaattcgatc acatatTTTT ttcgtcattt
121 tcaatctcct ataattgtaa tgtattgttt aacgccgaaa catcatgatt gagcccattt
181 agccccgtgt gttggtctac ctttattcca atcataaaat cgatacttgt agaatgcagt
241 aatggatatt acggtaacaa ctgtaatat acgtgcgggt attgcctaca aggaagtgtg
301 tgcaatagac tgaatggaac ttgtgaaaat ggggtgatca accattttaa agaaccgaga
361 tgtgctgttt gtagagacgg attctacaac agtagatgca cttctcaatg cggcaagtgt
421 gtgaacgatg agccttgtga taaagtaaca ggagaatgca ggaatggatg tcaacaacat
```

481 ttggaacctc ctttgtgtca gggtttgtaa tgatatatat attgtgtact gatatgcacg
 541 cttcaacgtg ttatatgata tattgcattc aaactgtctc atagcattga ccagcattgt
 601 aaagtcaaaa ctgcgttttg cattattaat gtatttcacg taatgaattt cctgtataca
 661 gttatgttaa cgtcttaaaa acacgcttta aactacacgt ccaaaataca tttatttgtg
 721 acctgtgtaa gaatatagat aaaataagta ggtttcttct taaccattaa aaacaaaaca
 781 atacaaaatc gtgtttaaac a

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LOCUS (LOC): CD646852 GenBank (R)
 GenBank ACC. NO. (GBN): CD646852
 GenBank VERSION (VER): CD646852.1 GI:31901304
 CAS REGISTRY NO. (RN): 537503-80-3
 SEQUENCE LENGTH (SQL): 572
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 18 Jun 2003
 DEFINITION (DEF): AUF_106_F02_T7 Crassostrea virginica Gonad Crassostrea virginica cDNA 5' similar to ***MEGF10*** protein, mRNA sequence.
 KEYWORDS (ST): EST
 SOURCE: Crassostrea virginica (eastern oyster)
 ORGANISM (ORGN): Crassostrea virginica
 Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Ostreoida; Ostreioidea; Ostreidae; Crassostrea
 NUCLEIC ACID COUNT (NA): 174 a 85 c 144 g 169 t
 COMMENT:

Contact: Liu ZJ
 The Fish Molecular Genetics and Biotechnology Laboratory,
 Department of Fisheries and Allied Aquacultures and Program of Cell
 and Molecular Biosciences
 Auburn University
 203 Swingle Hall, Auburn University, Auburn, AL 36849, USA
 Tel: 334 844 4054
 Fax: 334 844 9208
 Email: zliu@acesag.auburn.edu
 Seq primer: M13 Reverse.

REFERENCE: 1 (bases 1 to 572)
 AUTHOR (AU): Peatman,E.; Kucuktas,H.; Li,P.; He,C.; Feng,J.; Wei,X.; Liu,Z.
 TITLE (TI): Differentially expressed oyster (Crassostrea virginica) genes after exposure to mercury
 JOURNAL (SO): Unpublished

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..572	/organism="Crassostrea virginica" /mol-type="mRNA" /db-xref="taxon:6565" /clone-lib="Crassostrea virginica Gonad" /note="Organ: Gonad; Vector: pSport1; Site-1: NotI; Site-2: SalI"

SEQUENCE (SEQ):
 1 gtgatagtgg atgtaaaccg ggctggaagg gacaatactg tcacgaacaa tgtcaatatg
 61 gcttctatgg acaggactgc ctacttacat gtaacgacaa atgtaacggg tgaacaatg
 121 tgaacgggta ctgtgataga ggatgtaaac caggctggaa gggggacaac tgtcaacaac
 181 aatgcatgtc tgacttttat ggcgaaaact gtagcagaaa ttgtggatat tgcttagatg
 241 gtagaacatg ccaccacata aatggcacat gtgaacaggg atgtaatccg gggtacaaag
 301 ctccattctg taacgaagag tgtgattttg gattctacgg aaatagatgc cttcaggaat
 361 gtgggttcatt ttgcaaaaata tcacgtgatt gtcattcatt gactggtttt tgtaaaaacg
 421 gctgtaaaag tggttggcaa ggaaaggatt gttttgaagt ttcgaaactt gaagacagta
 481 atacagattg gaaatcaaga ttttacggaa tgttgggggc gttcttcgta ttgttgattt
 541 tgatttgtct tcttattgcc taccatatta ta

L2 ANSWER 8 OF 13 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): CD034532 GenBank (R)
 GenBank ACC. NO. (GBN): CD034532
 GenBank VERSION (VER): CD034532.1 GI:30416370
 CAS REGISTRY NO. (RN): 514024-90-9
 SEQUENCE LENGTH (SQL): 471
 MOLECULE TYPE (CI): mRNA; linear

DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 7 May 2003
DEFINITION (DEF): mgmt016xK13f.b Mated culture Magnaporthe grisea cDNA
clone mgmt016xK13 5', mRNA sequence.
KEYWORDS (ST): EST
SOURCE: Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM (ORGN): Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Sordariomycetes; Sordariomycetes incertae sedis;
Magnaporthaceae; Magnaporthe
NUCLEIC ACID COUNT (NA): 116 a 125 c 91 g 139 t

COMMENT:
Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact person
;Best nr hit (April. 22, 2003) ref|XP_236337.1| similar to ***MEGF10***
protein [Homo sapiens] [Rattu... 33 1.2
PCR Primers
FORWARD: T3 primer
BACKWARD: T7 primer
Plate: mgmt016 row: K column: 13
Seq primer: T3.

REFERENCE: 1 (bases 1 to 471)
AUTHOR (AU): Ebbole,D.J.; Yuan,J.; Thomas,T.L.; Bobrowicz,P.; Lu,G.;
Bhatterai,K. ; Dean,R.A.
TITLE (TI): Expressed sequence tags from the rice blast fungus,
Magnaporthe grisea
JOURNAL (SO): Unpublished (2002)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..471	/organism="Magnaporthe grisea" /strain="4091-5-8 X 4136-4-3" /db-xref="taxon:148305" /clone="mgmt016xK13" /clone-lib="Mated culture" /sex="Mat1-2 and Mat1-1 mixed culture" /cell-type="mixed sexual development" /dev-stage="asci, ascospores, perithecia, mycelium" /note="Vector: pBluescriptSK; Site-1: EcoRI; Site-2: XhoI; Two mating types were co-cultivated over a filter paper on oatmeal agar medium. After three days at 25 C plates were transferred to 21 C. Perithecia with asci and ascospores formed at the beginning of the third week. Material was collected by scraping tissue from the filter paper. Sequences were processed by one of two methods. where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimmed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."

SEQUENCE (SEQ):
1 ggcttttctt tctttttcgt ttgaccagac ccaagccgca aatccatcca acgatatact
61 ttttcttctt tttttttcct ctcttttctt cgtaactct caccgaatta ctgccgacat
121 aggcttctta gtactagga cttctcttga aagcaggtac atcattctcg acccgaaacg
181 ccgaaaataa aatcgggatt tccgcgatcc gcgtttcgca ttttcaacga caaaccatta
241 ccaagaggag gactcggcct tatcaaaacc atcgcgctca tcctagaagt gctgctgttt

301 tctactacac caagaacact gcctcgctga atttatttagc gaacgaacga agatttctctg
 361 gcatgtcggg catcacacag gcaacggcca tggtggccaa gcgagctgat ggatgtcccg
 421 atggatacta ccggtctgga aactactgtt atcggggatc tggatggtac t

L2 ANSWER 9 OF 13 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BU493977 GenBank (R)
 GenBank ACC. NO. (GBN): BU493977
 GenBank VERSION (VER): BU493977.1 GI:22790235
 CAS REGISTRY NO. (RN): 453296-65-6
 SEQUENCE LENGTH (SQL): 257
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 1 Oct 2002
 DEFINITION (DEF): vaa03f07.y2 SV DOGRDA RD3 Canis familiaris cDNA 5' similar to gp|AAH20198.1|BC020198_1 similar to ***MEGF10*** protein [Homo ;, mRNA sequence.
 SOURCE: dog.
 ORGANISM (ORGN): Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis
 NUCLEIC ACID COUNT (NA): 67 a 65 c 60 g 65 t
 COMMENT:
 other_ESTs: vaa03f07.x2
 Contact: Skip Virgin
 RNA Expression in Diseased Tissues by RDA
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Library was constructed by Tianxiang Shen and Skip Virgin DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Skip Virgin (virgin@immunology.wustl.edu)
 Possible reversed clone: similarity on wrong strand
 Seq primer: -40RP from Gibco.
 REFERENCE: 1 (bases 1 to 257)
 AUTHOR (AU): Virgin,S.; Tianxiang,S.; Karst,S.; Wobus,C.; Lay,M.; Clifton,S.; Pape,D.; Marra,M.; Hillier,L.; Martin,J.; Wylie,T.; Dante,M.; Theising,B.; Bowers,Y.; Gibbons,M.; Ritter,E.; Bennett,J.; Ronko,I.; Tsagareishvili,R.; Maguire,L.; Kennedy,S.; Waterston,R.; Wilson,R.
 TITLE (TI): RNA Expression in Diseased Tissues by RDA
 JOURNAL (SO): Unpublished (2002)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..257	/organism="Canis familiaris" /db-xref="taxon:9615" /clone-lib="SV DOGRDA RD3" /tissue-type="Brain from a dog with encephalitis" /lab-host="DH5a" /note="Vector: pCR2.1-TOPO; PCR products were directly cloned into TA cloning vector (pre-cut vector pCR2.1-TOPO was purchased from Invitrogen) Average insert size is 300bp. Our Insert also have same adaptor sequence on both ends. The sequence of the adaptor is: 5'-ATACGTGCAGGCTGGTTACATCTG-3'."

SEQUENCE (SEQ):
 1 cacaggcact ggagcagttg gttccacccc agccaggctc aactgacag gtgtttggag
 61 caatgcagcg accatggaca catttatcag cacagtgggg gacacacatt tccctgcttt
 121 cataaaatcc aggacaacac tgggatttgc gcctatacat agttttctcc ccatgtcgat
 181 aggcagtcgc ataactgatt ctgtgccgtg tacatttaaa ccagttcaga atatcagtg
 241 agctggtgta gtagatt

L2 ANSWER 10 OF 13 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BU493770 GenBank (R)

GenBank ACC. NO. (GBN): BU493770
 GenBank VERSION (VER): BU493770.1 GI:22790028
 CAS REGISTRY NO. (RN): 453296-12-3
 SEQUENCE LENGTH (SQL): 311
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Expressed sequence tag
 DATE (DATE): 1 oct 2002
 DEFINITION (DEF): vaa03f07.x2 SV DOGRDA RD3 Canis familiaris cDNA 3' similar to gp|BAB47409.1|AB058676_1 ***MEGF10*** protein ;, mRNA sequence.
 SOURCE: dog.
 ORGANISM (ORGN): Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis
 NUCLEIC ACID COUNT (NA): 82 a 71 c 75 g 82 t 1 others
 COMMENT:
 other_ESTs: vaa03f07.y2
 Contact: Skip Virgin
 RNA Expression in Diseased Tissues by RDA
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Library was constructed by Tianxiang Shen and skip Virgin DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Skip Virgin (virgin@immunology.wustl.edu)
 Putative full length read
 vector to vector length is 312
 Possible reversed clone: similarity on wrong strand
 Seq primer: -40UP from Gibco.
 REFERENCE: 1 (bases 1 to 311)
 AUTHOR (AU): Virgin,S.; Tianxiang,S.; Karst,S.; Wobus,C.; Lay,M.; Clifton,S.; Pape,D.; Marra,M.; Hillier,L.; Martin,J.; Wylie,T.; Dante,M.; Theising,B.; Bowers,Y.; Gibbons,M.; Ritter,E.; Bennett,J.; Ronko,I.; Tsagareishvili,R.; Maguire,L.; Kennedy,S.; Waterston,R.; Wilson,R.
 TITLE (TI): RNA Expression in Diseased Tissues by RDA
 JOURNAL (SO): Unpublished (2002)

Feature Key	Location	Qualifier
source	1..311	/organism="Canis familiaris" /db-xref="taxon:9615" /clone-lib="SV DOGRDA RD3" /tissue-type="Brain from a dog with encephalitis" /lab-host="DH5a" /note="Vector: pCR2.1-TOPO; PCR products were directly cloned into TA cloning vector (pre-cut vector pCR2.1-TOPO was purchased from Invitrogen) Average insert size is 300bp. Our Insert also have same adaptor sequence on both ends. The sequence of the adaptor is: 5'-ATACGTGCAGGCTGGTTACATCTG-3'."

SEQUENCE (SEQ):
 1 tgatcaaatc tactacacca gctgcactga tattctgaac tggtttaa at gtacacggca
 61 cagaatcagt tatcggactg cctatcgaca tggggagaaa actatgtata ggcgcaaatc
 121 ccagtgttgt cctggatttt atgaaagcag ggaaatgtgt gtccccact gtgctgataa
 181 atgtgtccat ggtcgtcgca ttgctccaaa cacctgtcag tgtgagcctg gctgggggtg
 241 aaccaactgc tccagtgctt gtgatggtga tcagatgtaa ccagcctgca cgtataatca
 301 ctantgaatt c

L2 ANSWER 11 OF 13 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BM427205 GenBank (R)
 GenBank ACC. NO. (GBN): BM427205
 GenBank VERSION (VER): BM427205.1 GI:18432195
 CAS REGISTRY NO. (RN): 396916-69-1
 SEQUENCE LENGTH (SQL): 668

MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Expressed sequence tag
DATE (DATE): 30 Jan 2002
DEFINITION (DEF): pgf2n.pk006.a15 Normalized Chicken Abdominal Fat Library (pgf2n) Gallus gallus cDNA clone
pgf2n.pk006.a15 5' similar to gi|14192943
ref|NP_115822.1| ***MEGF10*** protein [Homo sapiens] gi|14724016 ref|XP_030163.1| ***MEGF10*** protein [Homo sapiens] dbj|BAB47409.1| (AB058676) ***MEGF10*** protein (KIAA1780) [Homo sapiens], mRNA sequence.

SOURCE: chicken.
ORGANISM (ORGN): Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus

NUCLEIC ACID COUNT (NA): 108 a 256 c 199 g 104 t 1 others
COMMENT:

Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
Email: cogburn@udel.edu, www.chickest.udel.edu.

REFERENCE: 1 (bases 1 to 668)
AUTHOR (AU): Cogburn, L.A.; Morgan, R.; Burnside, J.
TITLE (TI): ESTs from Normalized Chicken fat cDNA library-USDA/IFAFS Animal Genome Project
JOURNAL (SO): Unpublished (2002)

FEATURES (FEAT):		
Feature Key	Location	Qualifier
source	1..668	/organism="Gallus gallus" /strain="Commercial broiler, Ottawa Research Centre strains, commercial leghorn" /db-xref="taxon:9031" /clone="pgf2n.pk006.a15" /clone-lib="Normalized Chicken Abdominal Fat Library (pgf2n)" /sex="Male and Female" /tissue-type="Abdominal Fat" /dev-stage="Embryonic (d18,d19); post-hatch (d1,w3,w7,w9 ,w16,1yr)" /lab-host="E. coli EMDH10B" /note="Vector: pCMVSPORT6; Library made from equivalent pools of total RNA isolated from each developmental age (across strains); single pass sequencing from 5'-end"

SEQUENCE (SEQ):
1 ccaccccagc gaccccaacg tctgcagcta ctgggagagt tttacagtag cagtgaagga
61 gtcatacgcc aaaccccaca ttgtgacctc caccgagccc tgcactggga caccaggatt
121 gccacagtcc tgcccgcagc aaagggtcgt gtaccgcacg gactaccgac aggcggtgcg
181 caccgactac cgccggcgct accagtgtct cctgggctac tatgagagca gggacgcctg
241 cgtcccgcgc tgcacccagg agtgcgtcca cgggcggtgc gtggcccccg agcgttgcca
301 gtgtgagccg ggctggaggg gacacgactg ctccagcgcg tgtgatgagc gtttgtgggg
361 caagaactgc gagcaccact gtgactgcca ccacggggcc ccctgcaatc ccctgagtgg
421 ggtctgtgcc tgcccccttg gcttcacccc cccactgtgc caccagccct gcccgcccg
481 ctccactcgc cccgactgcc gctctcactg cccatgccac cacggggccc cctgcaacgc
541 ctccactggg gcctgcctct gccccccagg acttgctggc ccactctgtg aggtgctgtg
601 ccccgagggg acaccgtgcg gcacccactg cccctgccag aatgggggta tctgccaccc
661 ccnngcct

LOCUS (LOC): BC020198 GenBank (R)
GenBank ACC. NO. (GBN): BC020198
GenBank VERSION (VER): BC020198.1 GI:18044365
CAS REGISTRY NO. (RN): 381931-64-2
SEQUENCE LENGTH (SQL): 2267
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Primates

DATE (DATE): 16 Sep 2003
 DEFINITION (DEF): Homo sapiens ***MEGF10*** protein, mRNA (cDNA clone
 IMAGE:4904255), complete cds.
 SOURCE: Homo sapiens (human)
 ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo
 NUCLEIC ACID COUNT (NA): 543 a 548 c 631 g 545 t
 COMMENT:

Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Genome Sequence Centre,
 BC Cancer Agency, Vancouver, BC, Canada
 info@bcgsc.bc.ca
 Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
 Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
 Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
 Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
 Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
 Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
 Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
 George Yang, Scott Zuyderduyn, Marco Marra.
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 40 Row: o Column: 4
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 14192942
 This clone has the following problem: The cds is short compared to
 the longest cds in the locus.

REFERENCE: 1 (bases 1 to 2267)
 AUTHOR (AU): Strausberg,R.L.; Feingold,E.A.; Grouse,L.H.;
 Derge,J.G.; Klausner,R.D.; Collins,F.S.; Wagner,L.;
 Shenmen,C.M.; Schuler,G.D.; Altschul,S.F.; Zeeberg,B.;
 Buetow,K.H.; Schaefer,C.F.; Bhat,N.K.; Hopkins,R.F.;
 Jordan,H.; Moore,T.; Max,S.I.; Wang,J.; Hsieh,F.;
 Diatchenko,L.; Marusina,K.; Farmer,A.A.; Rubin,G.M.;
 Hong,L.; Stapleton,M.; Soares,M.B.; Bonaldo,M.F.;
 Casavant,T.L.; Scheetz,T.E.; Brownstein,M.J.;
 Usdin,T.B.; Toshiyuki,S.; Carninci,P.; Prange,C.;
 Raha,S.S.; Loquellano,N.A.; Peters,G.J.; Abramson,R.D.;
 Mullahy,S.J.; Bosak,S.A.; McEwan,P.J.; McKernan,K.J.;
 Malek,J.A.; Gunaratne,P.H.; Richards,S.; Worley,K.C.;
 Hale,S.; Garcia,A.M.; Gay,L.J.; Hulyk,S.W.;
 Villalon,D.K.; Muzny,D.M.; Sodergren,E.J.; Lu,X.;
 Gibbs,R.A.; Fahey,J.; Helton,E.; Kettelman,M.; Madan,A.;
 Rodrigues,S.; Sanchez,A.; Whiting,M.; Madan,A.;
 Young,A.C.; Shevchenko,Y.; Bouffard,G.G.;
 Blakesley,R.W.; Touchman,J.W.; Green,E.D.;
 Dickson,M.C.; Rodriguez,A.C.; Grimwood,J.; Schmutz,J.;
 Myers,R.M.; Butterfield,Y.S.; Krzywinski,M.I.;
 Skalska,U.; Smailus,D.E.; Schnerch,A.; Schein,J.E.;
 Jones,S.J.; Marra,M.A.

TITLE (TI): Generation and initial analysis of more than 15,000
 full-length human and mouse cDNA sequences
 JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 99 (26), 16899-16903
 (2002)

OTHER SOURCE (OS): CA 138:84323
 REFERENCE: 2 (bases 1 to 2267)
 AUTHOR (AU): Strausberg,R.
 TITLE (TI): Direct submission
 JOURNAL (SO): Submitted (19-DEC-2001) National Institutes of Health,
 Mammalian Gene Collection (MGC), Cancer Genomics
 Office, National Cancer Institute, 31 Center Drive,
 Room 11A03, Bethesda, MD 20892-2590, USA

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..2267	/organism="Homo sapiens" /mol-type="mRNA" /db-xref="taxon:9606" /clone="IMAGE:4904255"

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/tissue-type="Muscle,
rhabdomyosarcoma"
/clone-lib="NIH-MGC-17"
/lab-host="DH10B-R"
/note="Vector: pOTB7"
/gene="MEGF10"
/note="synonym: KIAA1780"
/db-xref="LocusID:84466"
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/product="MEGF10 protein"
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/db-xref="GI:18044366"
/db-xref="LocusID:84466"
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GTASPLNLEDPNVCSHWESYSVTV
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EMCVPHCADKCVHGRCIAPNTCQCEPGWGGTNCS
SACGDGHWGPHCTSRCQCKNGALC
NPITGACHCAAGFRGWRCEDRCEQGTYGNDCHQR
CQCQNGATCDHVTGECRCPPGYTG
AFCEDLCPGKHGPQCEQRCPCQNGGVCHHVTGE
CSCPSGWMGTVCGQPCPEGRFGKN
CSQECQCHNGGTCDAAATGQCHCSPGYTGERCQDE
CPVGTYGVLCAETCQCVNGGKCYH
VSGACLCEAGFAGERCEARLCPEGLYGIKCDKRC
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KCTCAPGFKGIDCSTPCPLGTYGI
NCSSRCGCKNDVCSVPDGSCTCKAGWHGVDCSI
RCPSTGWGFGCNLTQCLNGGACN
TLDGTCTCAPGWRGEKCELPQDGTYGLNCAERC
DCSHADGCHPTTGHCRLPGWSGL F"

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gene 1..2267

CDS 280..1983

SEQUENCE (SEQ):

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1 aaactgggacg actgggaacg cgttgagacg ttcctctttc ccgcttctcc acctttacgc
61 ctgaaagaag actcccaaag attgctttct tctgggacgc tgcttgaacg ctaaccgcgt
121 tgattggaac agattttgtg tcttggtctg ctttgggtga agaccgggga gaaaagggtg
181 cgctgcgatt ctcaagatct ctggacctgg attatcattg caaatccatt aaagaaggag
241 aagcaagcgg atttcagaga ggttggtctt cagaaaaaaa tggttatttc tttgaactca
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421 taccacatc ctttgatca aatttactac acgagctgca ctgacattct aaactggttt
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541 tatagcgca agtctcagtg ttgtcctgga ttttatgaaa gcggggaaat gtgtgtcccc
601 cactgtgctg ataaatgtgt ccatggtcgc tgtattgtc caaacacctg tcagtgtgag
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901 ggggaatgcc gctgcccacc aggatacacc ggagccttct gtgaggatct ttgtcctcct
961 ggtaaacatg gtccacagtg tgagcagaga tgccttctgc aaaatggagg agtgtgtcat
1021 cacgtcactg gagaatgtc ttgcccttct ggctggatgg gcacagtgtg tggtcagcct
1081 tgcccagagg gtcgctttgg aaagaactgt tcccaagaat gccagtcca taatggaggg
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1381 tgtccctgcc acttggaaaa cactcatagc tgtcaccca tgtctggaga gtgtgcctgc
1441 aagccgggct ggtcaggact ctactgtaat gagacatgtt ctcttgatt ctacggggaa
1501 gcttgccagc agatctgcag ctgccaaaat ggggcagact gtgacagtgt gactggaaaag
1561 tgcacctgtg ccccaggatt caaaggaatt gactgctcta ccccatgccc tctgggaacc
1621 tatgggataa actgttcctc tcgctgtggc tgtaaaaatg atgcagtctg ctctcctgtg
1681 gacgggtctt gtacttgcaa ggcagggtgg cacggggtgg actgctccat cagatgtccc
1741 agtggcacat ggggctttgg ctgtaactta acatgccagt gcctcaacgg gggagcctgc
1801 aacaccctgg acgggacctg cacgtgtgca cctggatggc gcggggagaa atgcgaactt
1861 ccctgccagg atggcacgta cgggctgaac tgtgctgagc gctgcgactg cagccacgca
1921 gatggctgcc accctaccac gggccattgc cgtgcctcc ccgatggtc aggattgttt
1981 tgactattct gggctcattga atttccatgt gaatggtaac atcaatatgt taatttcac
2041 aaagaagcaa ggtggaatt taatggagat tgaatctata gatcaatttg ggaataactg
2101 tccacttaac aatatgaagt cttcagattc ataaacatgg gatgtcacca gcaacctctt
2161 cagtagtgtc tctcagcccc ttggaaaatg ttgagagctt ctttggtttc taaaggagta
2221 aactgagatg aactgtcaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa

```

LOCUS (LOC): AB058676 GenBank (R)
GenBank ACC. NO. (GBN): AB058676
GenBank VERSION (VER): AB058676.1 GI:14017776
CAS REGISTRY NO. (RN): 336671-12-6
SEQUENCE LENGTH (SQL): 7522
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Primates
DATE (DATE): 10 May 2001
DEFINITION (DEF): Homo sapiens mRNA for ***MEGF10*** protein (KIAA1780), complete cds.
SOURCE: Homo sapiens adult hippocampus cDNA to mRNA, clone:pf01012.
ORGANISM (ORGN): Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
NUCLEIC ACID COUNT (NA): 2130 a 1554 c 1697 g 2141 t
REFERENCE: 1 (sites)
AUTHOR (AU): Nagase,T.; Nakayama,M.; Nakajima,D.; Kikuno,R.; Ohara,O.
TITLE (TI): Prediction of the coding sequences of unidentified human genes. XX. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro
JOURNAL (SO): DNA Res., 8 (2), 85-95 (2001)
OTHER SOURCE (OS): CA 136:64933
REFERENCE: 2 (bases 1 to 7522)
AUTHOR (AU): Nakayama,M.; Nagase,T.; Nakajima,D.; Kikuno,R.; Ohara,O.
TITLE (TI): Direct Submission
JOURNAL (SO): Submitted (27-MAR-2001) Manabu Nakayama, Kazusa DNA Research Institute, Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:nmanabu@kazusa.or.jp, URL:http://www.kazusa.or.jp/huge, Tel:81-438-52-3915, Fax:81-438-52-3914)

FEATURES (FEAT):		
Feature Key	Location	Qualifier
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